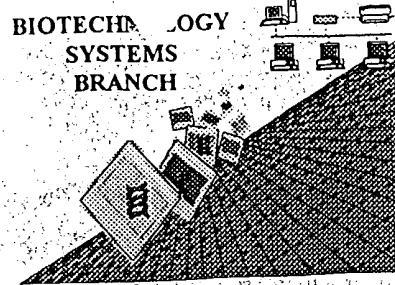**BEST AVAILABLE COPY**

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/825, 246_

Source: _OIPE_

Date Processed by STIC: _4-23-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/825,246_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or **Xaa** represents.

11 _____ Use of "Artificial" (NEW RULES)

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 ✓ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/825,246   TIME: 13:14:30

          Input Set : A:\0225-0033.20-SEQLIST.txt
          Output Set: N:\CRF3\04232001\I825246.raw

   4 <110> APPLICANT: Singh, Sharat
   5   Matray, Tracy
   6   Chenna, Ahmed
   8 <120> TITLE OF INVENTION: Sets of Oligonucleotide-Binding e-tag
   9   Probes
  11 <130> FILE REFERENCE: 0225-0033.20
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/825,246
C--> 14 <141> CURRENT FILING DATE: 2001-04-02
  16 <150> PRIOR APPLICATION NUMBER: US 09/698,846
  17 <151> PRIOR FILING DATE: 2000-10-27
  19 <150> PRIOR APPLICATION NUMBER: US 09/684,386
  20 <151> PRIOR FILING DATE: 2000-10-04
  22 <150> PRIOR APPLICATION NUMBER: US 09/602,586
  23 <151> PRIOR FILING DATE: 2000-06-21
  25 <150> PRIOR APPLICATION NUMBER: US 09/561,579
  26 <151> PRIOR FILING DATE: 2000-04-28
  28 <150> PRIOR APPLICATION NUMBER: US 09/303,029
  29 <151> PRIOR FILING DATE: 1999-04-30
  31 <160> NUMBER OF SEQ ID NOS: 18
  33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  35 <210> SEQ ID NO: 1
  36 <211> LENGTH: 16
  37 <212> TYPE: DNA
  38 <213> ORGANISM: Artificial Sequence
  40 <220> FEATURE:
  41 <223> OTHER INFORMATION: oligonucleotide
  43 <400> SEQUENCE: 1
  44 tcaccacatc ccagtg   16
  46 <210> SEQ ID NO: 2
  47 <211> LENGTH: 16
  48 <212> TYPE: DNA
  49 <213> ORGANISM: Artificial Sequence
  51 <220> FEATURE:
  52 <223> OTHER INFORMATION: oligonucleotide
  54 <400> SEQUENCE: 2
  55 gagggaggtt tggctg   16
  57 <210> SEQ ID NO: 3
  58 <211> LENGTH: 22
  59 <212> TYPE: DNA
  60 <213> ORGANISM: Artificial Sequence
  62 <220> FEATURE:
  63 <223> OTHER INFORMATION: oligonucleotide
  65 <221> NAME/KEY: misc_feature
  66 <222> LOCATION: (22)...(22)
  67 <223> OTHER INFORMATION: 3' nucleotide linked to tetramethyl rhodamine
  69 <400> SEQUENCE: 3
  70 ccagcaacca atgatgcccg tt   22

[handwritten annotation:] More specific response needed. What is the source of the artificial sequence?

[handwritten annotation:] See #12 on the Error Summary Sheet.

[stamp:] Does Not Comply Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/825,246   TIME: 13:14:30

Input Set : **A:\0225-0033.20-SEQLIST.txt**
Output Set: **N:\CRF3\04232001\I825246.raw**

```
 72 <210> SEQ ID NO: 4
 73 <211> LENGTH: 22
 74 <212> TYPE: DNA
 75 <213> ORGANISM: Artificial Sequence
 77 <220> FEATURE:
 78 <223> OTHER INFORMATION: oligonucleotide        See p. 1
 80 <221> NAME/KEY: misc_feature
 81 <222> LOCATION: (1)...(1)
 82 <223> OTHER INFORMATION: 5' nucleotide linked to fluorescein
 84 <221> NAME/KEY: misc_feature
 85 <222> LOCATION: (22)...(22)
 86 <223> OTHER INFORMATION: 3' nucleotide linked to tetramethyl rhodamine
 88 <400> SEQUENCE: 4
 89 ccagcaagca ctgatgcctg tt                                          22
 91 <210> SEQ ID NO: 5
 92 <211> LENGTH: 4
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Artificial Sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: peptide linker
 99 <400> SEQUENCE: 5
100 Lys Lys Ala Ala
101  1
103 <210> SEQ ID NO: 6
104 <211> LENGTH: 4
105 <212> TYPE: PRT
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: peptide linker
111 <400> SEQUENCE: 6
112 Lys Lys Lys Ala
113  1
115 <210> SEQ ID NO: 7
116 <211> LENGTH: 4
117 <212> TYPE: PRT
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: peptide linker
123 <400> SEQUENCE: 7
124 Lys Lys Lys Lys
125  1
127 <210> SEQ ID NO: 8
128 <211> LENGTH: 25
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: oligonucleotide         See p. 1
135 <400> SEQUENCE: 8
136 gaccaggaaa tagagaggaa atgta                                       25
```

RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/825,246   TIME: 13:14:30

Input Set : A:\0225-0033.20-SEQLIST.txt
Output Set: N:\CRF3\04232001\I825246.raw

```
138 <210> SEQ ID NO: 9
139 <211> LENGTH: 27
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: oligonucleotide
146 <400> SEQUENCE: 9
147 gaaggagaag gaagagttgg tattatc                    27
149 <210> SEQ ID NO: 10
150 <211> LENGTH: 21
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: oligonucleotide
157 <400> SEQUENCE: 10
158 ttgggctcag atctgtgata g                          21
160 <210> SEQ ID NO: 11
161 <211> LENGTH: 27
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: oligonucleotide
168 <400> SEQUENCE: 11
169 catctaggta tccaaaagga gagtcta                     27
171 <210> SEQ ID NO: 12
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: oligonucleotide
179 <400> SEQUENCE: 12
180 cggtatatag ttcttcctca tgctatt                     27
182 <210> SEQ ID NO: 13
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: oligonucleotide
190 <400> SEQUENCE: 13
191 gcaagatctt cgccttactg                             20
193 <210> SEQ ID NO: 14
194 <211> LENGTH: 32
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: probe
201 <221> NAME/KEY: misc_feature
202 <222> LOCATION: (1)...(1)
203 <223> OTHER INFORMATION: e-tag10s modification to the 5' nucleotide
```

```
205 <400> SEQUENCE: 14
206 ttccatttc tttttagagc agtatacaaa ga                                    32
208 <210> SEQ ID NO: 15
209 <211> LENGTH: 32
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: probe
216 <221> NAME/KEY: misc_feature
217 <222> LOCATION: (1)...(1)
218 <223> OTHER INFORMATION: e-tag10as modification to the 5' nucleotide
220 <400> SEQUENCE: 15
221 tctttgtata ctgctctaaa aagaaaatgg aa                                   32
223 <210> SEQ ID NO: 16
224 <211> LENGTH: 28
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: probe
231 <221> NAME/KEY: misc_feature
232 <222> LOCATION: (1)...(1)
233 <223> OTHER INFORMATION: e-tag11s modification to the 5' nucleotide
235 <400> SEQUENCE: 16
236 aaactccagc atagatgtgg atagcttg                                       28
238 <210> SEQ ID NO: 17
239 <211> LENGTH: 28
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: probe
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: (1)...(1)
248 <223> OTHER INFORMATION: e-tag11as modification to the 5' nucleotide
250 <400> SEQUENCE: 17
251 caagctatcc acatctatgc tggagttt                                       28
253 <210> SEQ ID NO: 18
254 <211> LENGTH: 23
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: probe
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: (1)...(1)
263 <223> OTHER INFORMATION: e-tag13as modification to the 5' nucleotide
265 <400> SEQUENCE: 18
266 aactgcttgt ggccatggct tag                                            23
```

VERIFICATION SUMMARY   DATE: 04/23/2001
PATENT APPLICATION: US/09/825,246   TIME: 13:14:31

Input Set : **A:\0225-0033.20-SEQLIST.txt**
Output Set: **N:\CRF3\04232001\I825246.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date